1600

RAW SEQUENCE LISTING   DATE: 09/12/2002
PATENT APPLICATION: US/10/080,980A   TIME: 10:15:41

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF4\09122002\J080980A.raw


```
   3  <110> APPLICANT: Bristol-Myers Squibb Company
   5  <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
   6        K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
   8  <130> FILE REFERENCE: D0121 NP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/080,980A
C--> 10 <141> CURRENT FILING DATE: 2002-02-21
  10  <150> PRIOR APPLICATION NUMBER: US 60/270,132
  11  <151> PRIOR FILING DATE: 2001-02-21
  13  <150> PRIOR APPLICATION NUMBER: US 60/278,953
  14  <151> PRIOR FILING DATE: 2001-03-27
  16  <160> NUMBER OF SEQ ID NOS: 74
  18  <170> SOFTWARE: PatentIn version 3.0
  20  <210> SEQ ID NO: 1
  21  <211> LENGTH: 2052
  22  <212> TYPE: DNA
  23  <213> ORGANISM: homo sapiens
  25  <220> FEATURE:
  26  <221> NAME/KEY: CDS
  27  <222> LOCATION: (121)..(1095)
  29  <400> SEQUENCE: 1
  30  cgtccggcgg ggcgcagggc tgagcgagcg tccgggctcc ggggctccgg ggaaggcggt      60
  32  tgcagctcct gagtgcagcg cggcttcctg ccactgtccc ggcccggcca cctctctgtc     120
  34  atg gct ctg gcg gac agc aca cgt gga tta ccc aac ggg ggc ggc ggc       168
  35  Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly Gly Gly Gly
  36  1               5                   10                  15
  38  ggg ggc ggc agt ggc tcc tcg tcg tcc tcc gcg gag cca ccg ctc ttc       216
  39  Gly Gly Gly Ser Gly Ser Ser Ser Ser Ser Ala Glu Pro Pro Leu Phe
  40              20                  25                  30
  42  ccc gac atc gtg gag ctg aac gtg ggg ggc cag gtg tac gtg acc cgg       264
  43  Pro Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg
  44              35                  40                  45
  46  cgc tgc acg gtg gtg tcg gtg ccc gac tcg ctg ctc tgg cgc atg ttc       312
  47  Arg Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe
  48          50                  55                  60
  50  acg cag cag cag ccg cag gag ctg gcc cgg gac agc aaa ggc cgc ttc       360
  51  Thr Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe
  52  65                  70                  75                  80
  54  ttt ctg gac cgg gac ggc ttc ctc ttc cgc tac atc ctg gat tac ctg       408
  55  Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
  56                  85                  90                  95
  58  cgg gac ttg cag ctc gtg ctg ccc gac tac ttc ccc gag cgc agc cgg       456
  59  Arg Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg
  60                  100                 105                 110
```

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62  ctg cag cgc gag gcc gag tac ttc gag ctg cca gag ctc gtg cgc cgc     504
63  Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg
64      115                 120                 125
66  ctc ggg gcg ccc cag cag ccc ggc ccg ggg ccg ccg ccc tcg cgg cgc     552
67  Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro Pro Pro Ser Arg Arg
68      130                 135                 140
70  ggg gtg cac aag gag ggc tcg ctg ggt gac gag ctg ctg ccg ctt ggc     600
71  Gly Val His Lys Glu Gly Ser Leu Gly Asp Glu Leu Leu Pro Leu Gly
72  145                 150                 155                 160
74  tac tcg gag ccc gaa cag cag gag ggc gcc tct gcc ggg gcg ccg tcg     648
75  Tyr Ser Glu Pro Glu Gln Gln Glu Gly Ala Ser Ala Gly Ala Pro Ser
76                  165                 170                 175
78  ccc acg ctg gag ctg gct agc cgc agt ccg tcc ggg ggc gcg gcg ggc     696
79  Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser Gly Gly Ala Ala Gly
80              180                 185                 190
82  ccg ctg ctc acg ccg tcc cag tcg ctg gac ggc agc cgg cgc tcg ggc     744
83  Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly
84          195                 200                 205
86  tac atc acc atc ggc tac cgc ggc tcc tac acc atc ggg cgg gac gcg     792
87  Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr Ile Gly Arg Asp Ala
88      210                 215                 220
90  cag gcg gac gcc aag ttc cgg cga gtg gcg cgc atc acc gtt tgc gga     840
91  Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg Ile Thr Val Cys Gly
92  225                 230                 235                 240
94  aag acg tcg ctg gcc aag gag gtg ttt ggg gac acc ctg aac gaa agc     888
95  Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp Thr Leu Asn Glu Ser
96                  245                 250                 255
98  cgg gac ccc gac cgt ccc ccg gag cgc tac acc tcg cgc tat tac ctc     936
99  Arg Asp Pro Asp Arg Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu
100                 260                 265                 270
102 aag ttc aac ttc ctg gag cag gcc ttc gac aag ctg tcc gag tcg ggc     984
103 Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys Leu Ser Glu Ser Gly
104             275                 280                 285
106 ttc cac atg gtg gcg tgc agc tcc acg ggc acc tgc gcc ttt gcc agc     1032
107 Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser
108     290                 295                 300
110 agc acc gac cag agc gag gac aag atc tgg acc agc tac acc gag tac     1080
111 Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr
112 305                 310                 315                 320
114 gtc ttc tgc agg gag tgagctcccc agacccctc gccactccag cgcccagtcc     1135
115 Val Phe Cys Arg Glu
116                 325
118 ttctcctgcc cgagagatga ttacagagcc tcttgtccca cctttgtccc ctggctgctg   1195
120 ccctcccatt ctccccctcc agtagtagct gggtgagacc tgtccgccca ccttccctcc   1255
122 actacagaac ctgcagccgc aaatcctctg ggctgcttcg tcttctttgg acctcctgaa   1315
124 ccgagagaac ccagaggaac ccccacccca ccccacctta ccactccatg ctttctctac   1375
126 tccctgcctc aaaccacccc tcccccagat ggtacttcag tttggatcta ttgggggagt   1435
128 gtggccacag accggggggat gattgaattg ttcagaacct gatttgaccg tgtccaatgt   1495
130 gcggaagatt tccttgaaat cttctcaagc tcttatgact cactggggggt ttaagagatc   1555
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          Input Set : A:\PTO.VSK.txt
          Output Set: N:\CRF4\09122002\J080980A.raw

132 aggattggtt ccactgtctg gggttagtgt tttacaaggt cattacacag tcttttgac  1615
134 ctcttttgaa ggtagagttt tagaaggctg gatggaagat tctgagcctg gaattaggac  1675
136 cccatggagg cagtcctcaa accacccctc ccccagatgg tacttcagtt tggatctatt  1735
138 ggggggagtgt ggccacagac cggggggatga ttgaattgtt cagaacctga ttggaccgtg  1795
140 tccaatgtgc ggaagatttc cttgaaatct tctcaagctc ttatgactca ctggggtttt  1855
142 aagagatcag gattggttcc actgtctggg gttagtgttt tacaaggtca ttacacagtc  1915
144 tttttgacct cttttgaagg tagagtttta gaaggctgga tggaagattc tgagcctgga  1975
146 attaggaccc catggaggca gttcagtaac taaactaata aagttttgaa aagttacacg  2035
148 taaaaaaaaa aaaaaaa                                                  2052
151 <210> SEQ ID NO: 2
152 <211> LENGTH: 325
153 <212> TYPE: PRT
154 <213> ORGANISM: homo sapiens
156 <400> SEQUENCE: 2
158 Met Ala Leu Ala Asp Ser Thr Arg Gly Leu Pro Asn Gly Gly Gly Gly
159 1               5                   10                  15
162 Gly Gly Gly Ser Gly Ser Ser Ser Ser Ser Ala Glu Pro Pro Leu Phe
163             20                  25                  30
166 Pro Asp Ile Val Glu Leu Asn Val Gly Gly Gln Val Tyr Val Thr Arg
167         35                  40                  45
170 Arg Cys Thr Val Val Ser Val Pro Asp Ser Leu Leu Trp Arg Met Phe
171     50                  55                  60
174 Thr Gln Gln Gln Pro Gln Glu Leu Ala Arg Asp Ser Lys Gly Arg Phe
175 65                  70                  75                  80
178 Phe Leu Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
179                 85                  90                  95
182 Arg Asp Leu Gln Leu Val Leu Pro Asp Tyr Phe Pro Glu Arg Ser Arg
183             100                 105                 110
186 Leu Gln Arg Glu Ala Glu Tyr Phe Glu Leu Pro Glu Leu Val Arg Arg
187         115                 120                 125
190 Leu Gly Ala Pro Gln Gln Pro Gly Pro Gly Pro Pro Pro Ser Arg Arg
191     130                 135                 140
194 Gly Val His Lys Glu Gly Ser Leu Gly Asp Glu Leu Leu Pro Leu Gly
195 145                 150                 155                 160
198 Tyr Ser Glu Pro Glu Gln Gln Glu Gly Ala Ser Ala Gly Ala Pro Ser
199                 165                 170                 175
202 Pro Thr Leu Glu Leu Ala Ser Arg Ser Pro Ser Gly Gly Ala Ala Gly
203             180                 185                 190
206 Pro Leu Leu Thr Pro Ser Gln Ser Leu Asp Gly Ser Arg Arg Ser Gly
207         195                 200                 205
210 Tyr Ile Thr Ile Gly Tyr Arg Gly Ser Tyr Thr Ile Gly Arg Asp Ala
211     210                 215                 220
214 Gln Ala Asp Ala Lys Phe Arg Arg Val Ala Arg Ile Thr Val Cys Gly
215 225                 230                 235                 240
218 Lys Thr Ser Leu Ala Lys Glu Val Phe Gly Asp Thr Leu Asn Glu Ser
219                 245                 250                 255
222 Arg Asp Pro Asp Arg Pro Pro Glu Arg Tyr Thr Ser Arg Tyr Tyr Leu
223             260                 265                 270
226 Lys Phe Asn Phe Leu Glu Gln Ala Phe Asp Lys Leu Ser Glu Ser Gly
```

```
227          275                      280                      285
230  Phe His Met Val Ala Cys Ser Ser Thr Gly Thr Cys Ala Phe Ala Ser
231       290                      295                      300
234  Ser Thr Asp Gln Ser Glu Asp Lys Ile Trp Thr Ser Tyr Thr Glu Tyr
235  305                      310                      315                      320
238  Val Phe Cys Arg Glu
239                      325
242  <210> SEQ ID NO: 3
243  <211> LENGTH: 228
244  <212> TYPE: PRT
245  <213> ORGANISM: Drosophila melanogaster
247  <400> SEQUENCE: 3
249  Met Pro Glu Ile Ile Glu Leu Asn Val Gly Gly Val Ser Tyr Thr Thr
250  1                      5                      10                      15
252  Thr Leu Ala Thr Leu Leu Gln Asp Lys Ser Thr Leu Leu Ala Glu Leu
253       20                      25                      30
255  Phe Gly Glu Gly Arg Asp Ser Leu Ala Lys Asp Ser Lys Gly Arg Tyr
256       35                      40                      45
258  Phe Leu Asp Arg Asp Gly Val Leu Phe Arg Tyr Ile Leu Asp Phe Leu
259       50                      55                      60
261  Arg Asp Lys Ala Leu His Leu Pro Glu Gly Phe Arg Glu Arg Gln Arg
262  65                      70                      75                      80
264  Leu Leu Arg Glu Ala Glu His Phe Lys Leu Thr Ala Met Leu Glu Cys
265       85                      90                      95
267  Ile Arg Ser Glu Arg Asp Ala Arg Pro Pro Gly Cys Ile Thr Ile Gly
268       100                      105                      110
270  Tyr Arg Gly Ser Phe Gln Phe Gly Lys Asp Gly Leu Ala Asp Val Lys
271       115                      120                      125
273  Phe Arg Lys Leu Ser Arg Ile Leu Val Cys Gly Arg Val Ala Gln Cys
274       130                      135                      140
276  Arg Glu Val Phe Gly Asp Thr Leu Asn Glu Ser Arg Asp Pro Asp His
277  145                      150                      155                      160
279  Gly Gly Thr Asp Arg Tyr Thr Ser Arg Phe Phe Leu Lys His Cys Tyr
280       165                      170                      175
282  Ile Glu Gln Ala Phe Asp Asn Leu His Asp His Gly Tyr Arg Met Ala
283       180                      185                      190
285  Gly Ser Cys Gly Ser Gly Thr Ala Gly Ser Ala Ala Glu Pro Lys Pro
286       195                      200                      205
288  Gly Val Asp Thr Glu Glu Asn Arg Trp Asn His Tyr Asn Glu Phe Val
289       210                      215                      220
291  Phe Ile Arg Asp
292  225
294  <210> SEQ ID NO: 4
295  <211> LENGTH: 435
296  <212> TYPE: PRT
297  <213> ORGANISM: Homo sapiens
299  <400> SEQUENCE: 4
301  Gln Gln Gln Lys Lys Gly Thr Met Ala Leu Ser Gly Asn Cys Ser Arg
302  1                      5                      10                      15
```

```
304 Tyr Tyr Pro Arg Glu Gln Gly Ser Ala Val Pro Asn Ser Phe Pro Glu
305         20                  25              30
307 Val Val Glu Leu Asn Val Gly Gly Gln Val Tyr Phe Thr Arg His Ser
308         35                  40              45
310 Thr Leu Ile Ser Ile Pro His Ser Leu Leu Trp Lys Met Phe Ser Pro
311     50                  55              60
313 Lys Arg Asp Thr Ala Asn Asp Leu Ala Lys Asp Ser Lys Gly Arg Phe
314 65                  70              75                  80
316 Phe Ile Asp Arg Asp Gly Phe Leu Phe Arg Tyr Ile Leu Asp Tyr Leu
317             85                  90                  95
319 Arg Asp Arg Gln Val Val Leu Pro Asp His Phe Pro Glu Lys Gly Arg
320             100             105             110
322 Leu Lys Arg Glu Ala Glu Tyr Phe Gln Leu Pro Asp Leu Val Lys Leu
323         115                 120             125
325 Leu Thr Pro Asp Glu Ile Lys Gln Ser Pro Asp Glu Phe Cys His Ser
326     130                 135             140
328 Asp Phe Glu Asp Ala Ser Gln Gly Ser Asp Thr Arg Ile Cys Pro Pro
329 145                 150             155                 160
331 Ser Ser Leu Leu Pro Ala Asp Arg Lys Trp Gly Phe Ile Thr Val Gly
332             165             170                 175
334 Tyr Arg Gly Ser Cys Thr Leu Gly Arg Glu Gly Gln Ala Asp Ala Lys
335             180             185             190
337 Phe Arg Arg Val Pro Arg Ile Leu Val Cys Gly Arg Ile Ser Leu Ala
338         195             200             205
340 Lys Glu Val Phe Gly Glu Thr Leu Asn Glu Ser Arg Asp Pro Asp Arg
341     210             215             220
343 Ala Pro Glu Arg Tyr Thr Ser Arg Phe Tyr Leu Lys Phe Lys His Leu
344 225             230             235                 240
346 Glu Arg Ala Phe Asp Met Leu Ser Glu Cys Gly Phe His Met Val Ala
347             245             250             255
349 Cys Asn Ser Ser Val Thr Ala Ser Phe Ile Asn Gln Tyr Thr Asp Asp
350             260             265             270
352 Lys Ile Trp Ser Ser Tyr Thr Glu Tyr Val Phe Tyr Arg Glu Pro Ser
353         275             280             285
355 Arg Trp Ser Pro Ser His Cys Asp Cys Cys Cys Lys Asn Gly Lys Gly
356     290             295             300
358 Asp Lys Glu Gly Glu Ser Gly Thr Ser Cys Asn Asp Leu Ser Thr Ser
359 305             310             315                 320
361 Ser Cys Asp Ser Gln Ser Glu Ala Ser Ser Pro Gln Glu Thr Val Ile
362             325             330             335
364 Cys Gly Pro Val Thr Arg Gln Thr Asn Ile Gln Thr Leu Asp Arg Pro
365         340             345             350
367 Ile Lys Lys Gly Pro Val Gln Leu Ile Gln Gln Ser Glu Met Arg Arg
368         355             360             365
370 Lys Ser Asp Leu Leu Arg Thr Leu Thr Ser Gly Ser Arg Glu Ser Asn
371     370             375             380
373 Met Ser Ser Lys Lys Lys Ala Val Lys Glu Lys Leu Ser Ile Glu Glu
374 385             390             395             400
376 Glu Leu Glu Lys Cys Ile Gln Asp Phe Leu Lys Ile Lys Ile Pro Asp
```

```
        RAW SEQUENCE LISTING ERROR SUMMARY        DATE: 09/12/2002
        PATENT APPLICATION:   US/10/080,980A         TIME: 10:15:42

        Input Set : A:\PTO.VSK.txt
        Output Set: N:\CRF4\09122002\J080980A.raw
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:6; Xaa Pos. 15
Seq#:8;  N Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159,160
Seq#:8;  N Pos. 161,162,163,164,165,166,167,488,489,490,491,492,493,494,495
Seq#:8;  N Pos. 496,497,498,499,500,501,502,503,504,505,506,507,508,509,510
Seq#:8;  N Pos. 511,512,513,514,515,516,517,518,519,520,521,522,523,524,525
Seq#:8;  N Pos. 526,527,528,529,530,531,532,533,534,535,536,537,538,539,540
Seq#:8;  N Pos. 541,542,543,544,545,546,670,671,672,673,674,675,676,677,678
Seq#:8;  N Pos. 679,680,681,682,683,684,685,686,687,688
```

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/10/080,980A

DATE: 09/12/2002
TIME: 10:15:42

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF4\09122002\J080980A.raw

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:6; Xaa Pos. 15
Seq#:8; N Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159,160
Seq#:8; N Pos. 161,162,163,164,165,166,167,488,489,490,491,492,493,494,495
Seq#:8; N Pos. 496,497,498,499,500,501,502,503,504,505,506,507,508,509,510
Seq#:8; N Pos. 511,512,513,514,515,516,517,518,519,520,521,522,523,524,525
Seq#:8; N Pos. 526,527,528,529,530,531,532,533,534,535,536,537,538,539,540
Seq#:8; N Pos. 541,542,543,544,545,546,670,671,672,673,674,675,676,677,678
Seq#:8; N Pos. 679,680,681,682,683,684,685,686,687,688

VERIFICATION SUMMARY   DATE: 09/12/2002
PATENT APPLICATION: US/10/080,980A   TIME: 10:15:42

        Input Set : A:\PTO.VSK.txt
        Output Set: N:\CRF4\09122002\J080980A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:547 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:120
L:559 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:480
L:561 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:540
L:565 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:660